Docket No.: PF-0346-2 CPA

1.25

http://patents.incyte.com:8000/cgi-bin/SeqServer/SeqServer Exhibit A

> SeqServer® biology in silico

Help

Sequences

BLAST2 Search Results

Phrap ClustalW 606 Assembly FASTA BLAST2 BLAST 2 Manu Retrieval

Translation

Sonfidential -- Property of Incyte Corporation SeqServer Version 4.6 Jan 2002

Program: blastp

Sequence ID(8):

983910CD1 vs. <u>genpept136</u>

NCBI-BLASTP 2.0.10 [Aug-26-1999]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghul Zhang, Zheng Thang, Webb Miller, and David J. Ligman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:1389-3402.

(314 letters) Query= 983910CD1

Database: genpept136

1,453,555 sequences; 449,659,834 total letters

.....done Searching

e-154 e-147 e-137 e-137 550 e-155 Score E (bits) Value 546 522 490 490 93002935 T cell receptor beta chain [Homo sapiens] T-cell receptor beta [Homo sapiens] Sequences producing significant alignments: 91100182

Score = 550 bits (1401), Expect = e-155 Identities = 272/311 (87%), Positives = 280/311 (89%), Gaps = 3/311 (0%)

Query: 1 MOTRILCWAALCLIGADHTCACVSCYTPSNRVTEXCKDVELRCDP1SGHTALWWTRGSLGG 60
MOTRIL W A CLICADHTCACVSCY+PSNRVTEXCKDVELRCDP1SGHTALWWTRGSLGG
Sbjct: 1 MOTRILLPWYAFCLLGADHTCACVSCSPSNRVTEXCKDVELRCDP1SGHTALWWTRGSLGG 60

Query: 61 GPEPLIYPQOTGAADDSGLMDRFFAVRPBGSVSTLKIQRTBQGDSAAYLRAGVAAGMSS 120 G EPLIYPQG A D SGLP+DRF A R GSVSTL IQRT+Q DSA YL A+ S Sbjct: 61 GLEFLIYPQGNSAPDRSGLPSDRFSAERTGGSVSTLFIQRTQQEDSAVYL----CASSLSL 117

Query: 121 YNEQYFCFCTRLTVLEDLKNVFPPEVAVFEPSEARISHTQKATLVCLATGFYPDHVELSW 180 Sbjet: 118 LSPLHFCANSTRLIVTEDLAKNFPPEVANFEPSEAEISHTQKATLVCLATGIFPDHVELSM 177 +FG GTRLTV EDL VFPPEVAVFEPSEAEISHTQKATLVCLATG +PDHVELSW

Query: 181 WANGKEVHSGVSTDPQPLABQPALADSRYCLSSRLAVSATFWQAPRAFFRAFGVQFYGLSE 240 WANGKEVHSGVSTDPQPLADGSRYCLSSRLAVSATFWQAPRAFFRAFFRCQVQFYGLSE

Sbjet: 178 WVNSKEVHSGVSTDPQPLKEQPALADSRYCLSSRLRVSATFWQNPRNHFRCQVQFYGLSE 237

Query: 241 NDEWTQDRAKFVTQTVSAEAWGRADCGPTSESYQQGVLSATILYEILLGKATLYAVLVSA 300 NDEWTODRAKEVTOJISAEAMGRADCGFTS SYQQGVLSATILLYELLLGKAT+YAVLVSA Sbjct: 238 NDEWTODRAKEVTOJISAEAMGRADCGFTSVSYQQGVLSATILYELLLGKATMYAVLVSA 297

Query: 301 LVLMAMVKRKD 311

LVIAMAMVKRKD Sbjct: 298 LVIAMAMVKRKD 308

>q1100182 T-cell receptor beta (Homo sapiens)

Length = 311

+

Score = 546 bits (1391), Expect = e-154 Identities = 268/314 (85%), Positives = 282/314 (89%), Gaps = 3/314 (0%)

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Query: 1 MGTRLLCWAALCLLGADHTGAGVSQTPSNKVTEKGKDVELRCDPISGHTALYMYRQSLGQ 60

MGT LLCM ALCLIGADH GVSQ P +K+T++G++V RCDPIS H LYWYRQ+LQQ SDjct: 1 MGTSLLCMMALCLIGADHADTGVSQNFRHKITRRGQNVTFRCDPISEHRRLYWYRQTLQQ 60

GPEFLIYFQGTGAADDSGLFNDRFFAVRPBGSVSTLKIQRTEQGDSAAYLRAGVAAGWSS 120 Query: 61

GPEFL YPQ + S L +DNF A RP+GS STL+1GKTPGCDSA YL A ++ +S SDjct: 61 GPEFLTYFQNEAQLEKSRLLSDRFSARFKGSPSTLEIQRTPGCDSAMYLCA--SSPGTS 118

Query: 121 YNBQYFGPGTRLIVLEDLKNVP PPENAVFEPSBAEISHTQKATLVCLATGFYDDHVELSM 180 Y BQYFGPGTRLIV EDLKNVPPPENAVFEPSBAEISHTQKATLVCLATGFYDHVELSM Sbjct: 119 Y-BQYFGPGTRLIVTEDLKNVPPPENAVFEPSBAEISHTQKATLVCLATGFYPDHVELSM 177

Query: 181 WVNGKEVHSGVSTDPQPLKEQPALADSRYCLSSRLRVSATFWQNPRNHFRCQVQFYGLSE 240 Sbjet: 178 WVNGKEVHSGVSTDPQPLKEQPALADSRYCLSSRLRVSATFWQNPRNHFRCQVQFYGLSE 237 WVNGKEVHSGVSTIDPQPLKEQPALAIDSRYCLSSRLRVSATFWQNPRNHFRCQVQFYGLSE

Query: 241 NDEWTODRAKEVTQIVSAEAMGRADCGFTSESYQQGJLSATILYZILLGKATLYAULVSA 300 NDEWTODRAKEVTQIVSAEAMGRADCGFTSESYQQGJLSATILYZILLGKATLYAULVSA Sbjet: 238 NDEWTQDRAKEVTQIVSAEAMGRADCGFTSESYQGGJLSATILYZILLGKATLYAVLVSA 297

Query: 301 LVLMAMVKRKDSRG 314 LVLMAMVKRKDSRG

Sbjct: 298 LVLMAMVKRKDSRG 311

93339012 T-cell receptor precursor [Homo sapiens]

Score = 522 bits (1330), Expect = e-147 Identities = 254/311 (81%), Positives = 271/311 (86%), Gaps = 2/311 (0%)

BLAST2 Results

3 of 5

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Query: 181 WONGKEWHSGVSTDRQPLKEQPALADSRYCLSSRLRVSATFWQNFRNHFRCQVQPYGLSE 240 WINGKEWHSGVSTDRQPLKEQPALADSRYCLSSRLRVSATFWQNPRUHFRCQVQPYGLSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query: 121 YNEQYFGFOTRLIVLEDLKNVFPPEVAVFEPSEAEISHTQKATLVCLATGFYPDHVELSM 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E +PG GTRLIV+EDL VPPPEVAVPEPSEAEISHTQKATLVCLATGF+PDHVELSM SDjct: 118 AGBAFPGQGTRLIVVEDLAKVFPPEVAVPEPSEAEISHTQKATLVCLATGFPDHVELSW 177
                                                                                                                                                                                                                                                                                                            GPEFLIYFQGTGAADDSGLPNDRFFAVRPEGSVSTLKIQRTEQGDSAAYLRAGVAAGWSS 120
                                                                                                                                                                                                                                                                                                                                                   G E LIYP DDSG+P DRF A P S STLKIQ +E DSA Y A+ ++
Sbjct: 61 GLELLIYFWRNVPIDDSGAPEDRESANGHPASFSTLKIQPSERBSAVYF---CASSFNG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query: 241 NDEWTQDRAKFVTQIVSAEAWGRADCGFTSESYQQGVLSATILYEILLGKATLYAVLVSA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NDBATQDRAKPATQIVSAEAMGRADCGFTS SYQQGVLSATILYEILLGKATLYAVLVSA
Sbjct: 238 NDBATQDRAKPATQIVSAEAMGRADCGFTSVSYQQGVLSATILYEILLGKATLYAVLVSA 297
                                                                                                                                                                           M + C +LC+L A HT AGV Q+P ++VTB G++V LRC PISGH +L+WYRQ++ +
MDSWTPCCVSLCILVAKHTDAGVIQSPRHEVTERGQEVTLRCKPISGHNSLFWYRQTMRR 60
                                                                                                                                     Query: 1 MCTRLLCWAALCLLGADHTGAGVSQTPSNKVTFEKGKDVELRCDPISGHTALYWYRQSLGQ 60
    Score = 490 bits (1249), Expect = e-137
Identities = 241/311 (77%), Positives = 262/311 (83%), Gaps = 3/311 (0%)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sbjct: 178 WVNGKEVHSGVSTDPQPLKEQPALADSRYCLSSRLRVSATFWQNPRNHFRCQVQFYGLSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Number of HSP's better than 10.0 without gapping: 4379
Number of HSP's better than 10.0 without gapping: 4379
Number of HSP's that attempted gapping in prelim test: 13046
Number of HSP's gapped (non-prelim): 19060
Hughth of query: 314
length of database: 449,659,834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Number of sequences in database: 1,453,555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Posted date: Jul 31, 2003 9:27 AM Number of letters in database: 449,659,834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Number of sequences better than 10.0: 17425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Extension: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                effective length of query: 258
effective length of database: 568,260,754
effective search space: 95011274532
effective search space used: 95011274532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Number of extensions: 12787980
Number of successful extensions: 59096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matrix: BLOSUM62
Gap Penalties: Existence: 11, Ex
Number of Hits to DB: 297167763
Number of Sequences: 1453555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query: 301 LVLMAMVKRKD 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sbjct: 298 LVLMAMVKRKD 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      К Н
0.133 0.411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database: genpept136
Posted date: Jul 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVLMAMVKRKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gapped K H H 0.270 0.0470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.318
                                                                                                                                                                                                                                                                                                                 Query: 61
                                                                                                                                                                                                                           Sbjct: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lambda
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Y BQYFGFGTRUTV EDLKNVFPPENAVTEPSEAEISHTQKATIACLATGFYPDHVELSM
Sbjct: 119 Y-BQYFGFGTRUTVTEDLKNVFPPENAVPEPSEAEISHTQKATUVCLATGFYPDHVELSM 177
                                                                                                                                                                           GPEPLIYFQOTGAADDSGLRYDRFRAVRPBGSVSTLKIQRTBQGDSAAYLRAGVAAGMSS 120
GPEPL YFQ + S L +DRF A RP+GS STL+IQRTBQGDSA YL A AG +
                                                                                                                                                                                                                                                                                                                                                       Query: 121 YNBQYFGFGTRLTVLEDLANVFPPEVANFEPSEAEISHTQKATIJVCLATGFYPDHVELSW 180
Q+FG GTRL++LEDL VFPEVANFEPSEAEISHTQKATIJVCLATG +PDHVELSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WANGKEVHSGVSTDPQPLKBQPALADSRYCLSSRLRVSATFWQNPNHFRCQWQPYGLSE
Sbjct: 179 WYNGKEVHSGVSTDPQPLKBQPALADSRYCLSSRLRVSATFWQNPRHFRCQWQPYGLSE 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query: 61 GPEFLIYPQGTGAADDSGLENDRFFAVRPBGSVSTLKIQRTEGGDSAAYLRAGVAAGMSS 120
EFL+ F ++ S + +D+F RP+GS TLKI+ T+ DSA Y A ++ +S
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sbjet: 121 --PQHFGDGTRLSILEDLAKVFPFEVAVFEPSEABISHTOKATLVCLATGIFPDHVELSW 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query: 181 WVNGKEVHSGVSTDPQPLKEQPALADSRYCLSSRLRVSATFWQNFRNHFRCQVQFYGLSE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NDEWTQDRAKPVTQIVSAEAWGRADCGFTS SYQQGVLSATILYEILLGRAT+YAVLVSA Sbjct: 239 NDEWTQDRAKPVTQIVSAEAWGRADCGFTSVSYQQGVLSATILYEILLGRATMYAVLVSA 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sbjct: 61 KVEFLVSFYNNEISEKSEIFDDQFSVERPDGSNPTLKIRSTKLEDSAMYPCA--SSETNS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query: 181 WVNGKEVHSGVSTDPQPLKEQPALADSRYCLSSRLRVSATFWQNPRNHFRCQVQFYGLSE 240
                                                                                                                                                                                                                                                                 GPEFLIYFQNEAQLEKSRLLSDRFSAERPKGSFSTLEIQRTEQGDSAMYLCASSLAGLNQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query: 241 NDEWTQDRAKFVTQIVSAEAWGRADCGFTSESYQQGVLSATILYEILLGKATLYAVLVSA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sbjct: 178 WVNEXEVHSGVSTDPQPLKEQPALADSRYCLSSRLRVSATFWQNFRNHFRCQVQFYGLSE 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query: 241 NDEWIQDRAKPVIQIVSAEAWGRADCGFISESYQQGVLSATILYEILLGKATLYAVLVSA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NDBATQDRAKPYTQIVSABAMGRADCGFTSBSYQQOVLSATILLYBILLGRATLYAVLVSA
Sbjct: 238 NDBATQDRAKPYTQIVSABAMGRADCGFTSBSYQQGVLSATILYBILLGRATLYAVLVSA 297
MSTRLLCMAALCLLGADHTGACVSQTPSUKVTEKGUDVELACDP1SGHTALYWTRQSLQQ 60
MGT LLCM ALCLLGADH GVSQ P + +7++6++V RCDP1S H LYWYRQ+LQQ
MGTSLLCMMALCLLGADHADTGVSQNFRHNTTKRQQNVTFRCDP1SEHRRLYWTRQTLGQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query: 1 MOTRILCMAALCLIAGADHTGAGYSQTPSNRVTEXGEXDDFLEGETTALYWYRQSLQQ 60
M T L+CMA LL A T V+QTPS++VT+ C++V LRC P1S H YWYRQ LQQ
Sbjct: 1 MDYMLVCMAIFSLLKAGLTEPBUYQTPSRQVTQMSQEYILRCVPISNHLXFYWYRQILQQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score = 490 bits (1249), Expect = e-137
Identities = 248/314 (78%), Positives = 267/314 (84%), Gaps = 3/314 (0%)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WANCKEVHSGVSTDPQPLKEQPALADSRYCLSSRLRVSATFWQNPRNHFRCQVQFYGLSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ><u>022469288</u> T cell receptor beta chain BV12S1 J1-1 BC1 [Homo sapiens]
Length = 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2g5741519 unnamed protein product [unidentified]
Length = 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query: 301 LVLMAMVKRKDSRG 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sbjct: 298 LVLMAMVKRKDSRG 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query: 301 LVLMAMVRRKD 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sbjct: 299 LVLMAMVKRKD 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVLMAMVKRKD
                                                                                                                                                                                                                                                                      Sbjct: 61
                                                                                                                                                                                Query: 61
    Query: 1
                                                                                     Sbjct: 1
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4 of 5

8/28/03 9:56 AM

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T: 11 A: 40 X1: 16 (7.3 bits) X2: 38 (14.8 bits) X3: 64 (24.9 bits) S1: 41 (21.7 bits)

Submit sequences to: BLAST2 🗷 Submit Reset

IncyteGenomics

8/28/03 9:56 AM